

SEQUENCE LISTING

<110> SERVANT, GUY
 CHANG, HONG
 REDCROW, CYRIL
 RAY, SUMITA
 CLARK, IMRAN

<120> IMPROVED ELECTROPHYSIOLOGICAL ASSAYS USING OOCYTES THAT
 EXPRESS HUMAN ENaC AND THE USE OF PHENAMIL TO IMPROVE
 THE EFFECT OF ENaC ENHANCERS IN ASSAYS USING MEMBRANE
 POTENTIAL REPORTING DYES

<130> 67824.431530

<140> 10/563,758

<141> 2006-01-09

<150> PCT/US04/021853

<151> 2004-07-09

<150> 60/485,745

<151> 2003-07-10

<150> 10/133,573

<151> 2002-04-29

<150> 60/287,413

<151> 2001-05-01

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<170> PatentIn Ver. 3.3

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<212> DNA

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Val Ser Leu Ser Val Gly Phe Lys Thr Met Asp Phe Pro Ala Val Thr
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 Cys Gln Ser Val Cys Lys Glu Ala Cys Ser Phe Lys Glu Trp Thr Leu
 450 455 460
 Thr Thr Ser Leu Ala Gln Trp Pro Ser Val Val Ser Glu Lys Trp Leu
 465 470 475 480
 Leu Pro Val Leu Thr Trp Asp Gln Gly Arg Gln Val Asn Lys Lys Leu
 485 490 495
 Asn Lys Thr Asp Leu Ala Lys Leu Leu Ile Phe Tyr Lys Asp Leu Asn
 500 505 510
 Gln Arg Ser Ile Met Glu Ser Pro Ala Asn Ser Ile Glu Met Leu Leu
 515 520 525
 Ser Asn Phe Gly Gly Gln Leu Gly Leu Trp Met Ser Cys Ser Val Val
 530 535 540
 Cys Val Ile Glu Ile Ile Glu Val Phe Phe Ile Asp Phe Phe Ser Ile
 545 550 555 560
 Ile Ala Arg Arg Gln Trp Gln Lys Ala Lys Glu Trp Trp Ala Trp Lys
 565 570 575
 Gln Ala Pro Pro Cys Pro Glu Ala Pro Arg Ser Pro Gln Gly Gln Asp
 580 585 590
 Asn Pro Ala Leu Asp Ile Asp Asp Asp Leu Pro Thr Phe Asn Ser Ala
 595 600 605

Leu His Leu Pro Pro Ala Leu Gly Thr Gln Val Pro Gly Thr Pro Pro
 610 615 620
 Pro Lys Tyr Asn Thr Leu Arg Leu Glu Arg Ala Phe Ser Asn Gln Leu
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 Thr Asp Thr Gln Met Leu Asp Glu Leu
 645

<210> 7
 <211> 1916
 <212> DNA
 <213> Homo sapiens

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 cccaaggagg ggcaccagga ggggctggtg gagctgcccg cctcgttccg ggagctgctc 180
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 aaccgcctca agacgacgtc ctgggggctg ctgtccctgg gagccctggg cgcgctctgc 300
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 acccgagacc cagcgggcct catctcccac gggatgatgt tccaggggtt ctggcgggag 1860
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<210> 8

<211> 638

<212> PRT

<213> Homo sapiens

<400> 8

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Gly Gly Ser His Leu Gln Ala Ala Ala Gln Thr Pro Pro Arg Pro Gly
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Pro Pro Ser Ala Pro Pro Pro Pro Pro Lys Glu Gly His Gln Glu Gly
 35 40 45

Leu Val Glu Leu Pro Ala Ser Phe Arg Glu Leu Leu Thr Phe Phe Cys
 50 55 60

Thr Asn Ala Thr Ile His Gly Ala Ile Arg Leu Val Cys Ser Arg Gly
 65 70 75 80

Asn Arg Leu Lys Thr Thr Ser Trp Gly Leu Leu Ser Leu Gly Ala Leu
 85 90 95

Val Ala Leu Cys Trp Gln Leu Gly Leu Leu Phe Glu Arg His Trp His
 100 105 110

Arg Pro Val Leu Met Ala Val Ser Val His Ser Glu Arg Lys Leu Leu
 115 120 125

Pro Leu Val Thr Leu Cys Asp Gly Asn Pro Arg Arg Pro Ser Pro Val
 130 135 140

Leu Arg His Leu Glu Leu Leu Asp Glu Phe Ala Arg Glu Asn Ile Asp
 145 150 155 160

Ser Leu Tyr Asn Val Asn Leu Ser Lys Gly Arg Ala Ala Leu Ser Ala
 165 170 175

Thr Val Pro Arg His Glu Pro Pro Phe His Leu Asp Arg Glu Ile Arg
 180 185 190

Leu Gln Arg Leu Ser His Ser Gly Ser Arg Val Arg Val Gly Phe Arg
 195 200 205

Leu Cys Asn Ser Thr Gly Gly Asp Cys Phe Tyr Arg Gly Tyr Thr Ser
 210 215 220

Gly Val Ala Ala Val Gln Asp Trp Tyr His Phe His Tyr Val Asp Ile
 225 230 235 240

Leu Ala Leu Leu Pro Ala Ala Trp Glu Asp Ser His Gly Ser Gln Asp
 245 250 255

Gly His Phe Val Leu Ser Cys Ser Tyr Asp Gly Leu Asp Cys Gln Ala
 260 265 270
 Arg Gln Phe Arg Thr Phe His His Pro Thr Tyr Gly Ser Cys Tyr Thr
 275 280 285
 Val Asp Gly Val Trp Thr Ala Gln Arg Pro Gly Ile Thr His Gly Val
 290 295 300
 Gly Leu Val Leu Arg Val Glu Gln Gln Pro His Leu Pro Leu Leu Ser
 305 310 315 320
 Thr Leu Ala Gly Ile Arg Val Met Val His Gly Arg Asn His Thr Pro
 325 330 335
 Phe Leu Gly His His Ser Phe Ser Val Arg Pro Gly Thr Glu Ala Thr
 340 345 350
 Ile Ser Ile Arg Glu Asp Glu Val His Arg Leu Gly Ser Pro Tyr Gly
 355 360 365
 His Cys Thr Ala Gly Gly Glu Gly Val Glu Val Glu Leu Leu His Asn
 370 375 380
 Thr Ser Tyr Thr Arg Gln Ala Cys Leu Val Ser Cys Phe Gln Gln Leu
 385 390 395 400
 Met Val Glu Thr Cys Ser Cys Gly Tyr Tyr Leu His Pro Leu Pro Ala
 405 410 415
 Gly Ala Glu Tyr Cys Ser Ser Ala Arg His Pro Ala Trp Gly His Cys
 420 425 430
 Phe Tyr Arg Leu Tyr Gln Asp Leu Glu Thr His Arg Leu Pro Cys Thr
 435 440 445
 Ser Arg Cys Pro Arg Pro Cys Arg Glu Ser Ala Phe Lys Leu Ser Thr
 450 455 460
 Gly Thr Ser Arg Trp Pro Ser Ala Lys Ser Ala Gly Trp Thr Leu Ala
 465 470 475 480
 Thr Leu Gly Glu Gln Gly Leu Pro His Gln Ser His Arg Gln Arg Ser
 485 490 495
 Ser Leu Ala Lys Ile Asn Ile Val Tyr Gln Glu Leu Asn Tyr Arg Ser
 500 505 510
 Val Glu Glu Ala Pro Val Tyr Ser Val Pro Gln Leu Leu Ser Ala Met
 515 520 525
 Gly Ser Leu Tyr Ser Leu Trp Phe Gly Ala Ser Val Leu Ser Leu Leu
 530 535 540

Glu Leu Leu Glu Leu Leu Leu Asp Ala Ser Ala Leu Thr Leu Val Leu
545 550 555 560

Gly Gly Arg Arg Leu Arg Arg Ala Trp Phe Ser Trp Pro Arg Ala Ser
565 570 575

Pro Ala Ser Gly Ala Ser Ser Ile Lys Pro Glu Ala Ser Gln Met Pro
580 585 590

Pro Pro Ala Gly Gly Thr Ser Asp Asp Pro Glu Pro Ser Gly Pro His
595 600 605

Leu Pro Arg Val Met Leu Pro Gly Val Leu Ala Gly Val Ser Ala Glu
610 615 620

Glu Ser Trp Ala Gly Pro Gln Pro Leu Glu Thr Leu Asp Thr
625 630 635

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 9

cgcggtatccg cccataaccag gtctcatg

28

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

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ccggaattcc tgcacatcct tcaatcttgc

30

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

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cgcggatcca gcaggtgcca ctatgcac 28

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 12
ccgctcgagg tcttggtgc tcagtgc 28

<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 13
cgcggatccc ctcaaagtc catcctcg 28

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 14
ccggaattcg actagatctg tcttctcaac 30